SEQ SEARCH SUMMARY

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: February 24, 2004, 01:09:42 ; Search time 4177.15 Seconds
                                            (without alignments)
                                            9795.148 Million cell updates/sec

Title: US-10-017-471B-19_COPY_1199_2142
Perfect score: 944
Sequence: 1 tcagccggagaacgcgggggc..........caaaactactgcttcgggca 944

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   GenEmbl:*
                 1: gb_ba:*
                 2: gb_htg:*
                 3: gb_in:*
                 4: gb_om:*
                 5: gb_ov:*
                 6: gb_pat:*
                 7: gb_ph:*
                 8: gb_pl:*
                 9: gb_pr:*
                 10: gb_ro:*
                 11: gb_sts:*
                 12: gb_sy:*
                 13: gb_un:*
                 14: gb_vi:*
                 15: em_ba:*
                 16: em_fun:*
                 17: em_hum:*
                 18: em_in:*
                 19: em_mu:*
                 20: em_om:*
                 21: em_or:*
                 22: em_ov:*
                 23: em_pat:*
                 24: em_ph:*
                 25: em_pl:*
                 26: em_ro:*
                 27: em_sts:*

SEQ 19 in DNA databases

```
28:  em_un:*
29:  em_vi:*
30:  em_htg_hum:*
31:  em_htg_inv:*
32:  em_htg_other:*
33:  em_htg_mus:*
34:  em_htg_pln:*
35:  em_htg_rod:*
36:  em_htg_mam:*
37:  em_htg_vrt:*
38:  em_sy:*
39:  em_htgo_hum:*
40:  em_htgo_mus:*
41:  em_htgo_other:*
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

                              SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	944	100.0	6727	1	SCO007731	AJ007731 Streptomy
c	2	944	100.0	290850	1	SCO939127	AL939127 Streptomy
c	3	513.6	54.4	1203	1	STMAFSAA	M24250 S.griseus a
c	4	513.6	54.4	12070	1	AB011413	AB011413 Streptomy
c	5	279	29.6	6252	1	SVU24659	U24659 Streptomyce
c	6	272.4	28.9	1215	1	AB001608	AB001608 Streptomy
c	7	254	26.9	210614	1	AB088224	AB088224 Streptomy
c	8	208.2	22.1	2234	1	AB001683	AB001683 Streptomy
c	9	178.2	18.9	92294	1	AY117439	AY117439 Streptomy
	10	121.4	12.9	300550	1	AP005030	AP005030 Streptomy
	11	95.2	10.1	9521	6	AX188771	AX188771 Sequence
c	12	95.2	10.1	9521	6	AX188772	AX188772 Sequence
	13	95.2	10.1	22918	1	SCO276673	AJ276673 Streptomy
c	14	95.2	10.1	178073	1	SCO590464	AL590464 Streptomy
c	15	74.6	7.9	299050	1	SCO939119	AL939119 Streptomy
c	16	70.6	7.5	181850	2	BX276102	BX276102 Danio rer
c	17	69.8	7.4	125020	9	AF429315	AF429315 Homo sapi
	18	69.6	7.4	293050	1	SCO939116	AL939116 Streptomy
c	19	69.4	7.4	300425	1	AP005022	AP005022 Streptomy
c	20	68.8	7.3	4725	6	AX697993	AX697993 Sequence
c	21	68.8	7.3	60196	6	AX697977	AX697977 Sequence
	22	68.4	7.2	299425	1	AP005037	AP005037 Streptomy
c	23	68.4	7.2	303450	1	SCO939130	AL939130 Streptomy
c	24	68	7.2	166634	2	AC141736	AC141736 Apis mell
c	25	67.6	7.2	64790	8	AP004863	AP004863 Oryza sat
c	26	67	7.1	15738	6	AX803762	AX803762 Sequence
c	27	67	7.1	61944	6	AX803750	AX803750 Sequence
	28	67	7.1	125020	9	AF429315	AF429315 Homo sapi
c	29	66.4	7.0	48000	1	POL505006	AJ505006 Sorangium
c	30	66.4	7.0	172650	2	AP005772	AP005772 Oryza sat
c	31	66.2	7.0	8113	14	HSBBICP4A	L14320 Bovine herp
	32	66.2	7.0	135301	14	BHV1CGEN	AJ004801 Bovine he
c	33	66.2	7.0	135301	14	BHV1CGEN	AJ004801 Bovine he

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OM nucleic - nucleic search, using sw model

Run on: February 24, 2004, 01:08:32 ; Search time 696.032 Seconds
                                               (without alignments)
                                               5761.655 Million cell updates/sec

Title: US-10-017-471B-19_COPY_1199_2142
Perfect score: 944
Sequence: 1 tcagccggagaacgcggggc..........caaaactactgcttcgggca 944

Scoring table: IDENTITY_NUC
                   Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   N_Geneseq_29Jan04:*
                   1: geneseqn1980s:*
                   2: geneseqn1990s:*
                   3: geneseqn2000s:*
                   4: geneseqn2001as:*
                   5: geneseqn2001bs:*
                   6: geneseqn2002s:*
                   7: geneseqn2003as:*
                   8: geneseqn2003bs:*
                   9: geneseqn2003cs:*
                   10: geneseqn2004s:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES
                      %
Result   Query
    No.   Score   Match Length DB   ID   Description
    ----
        1   944   100.0   4346 6   ABN86379   Abn86379 ScbA, Scb
        2   944   100.0   4346 9   ADE14794   Ade14794 Streptomy
        3   170   18.0   401 6   ABN86377   Abn86377 S. coelic
c   4   170   18.0   401 6   ABN86378   Abn86378 S. coelic
        5   170   18.0   401 9   ADE14790   Ade14790 Streptomy
        6   95.2   10.1   9521 4   AAS07627   Aas07627 Streptoco
c   7   82   8.7 114955 2   AAX53491   Aax53491 Human ade
        8   75.8   8.0 114955 2   AAX53491   Aax53491 Human ade

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OM nucleic - nucleic search, using sw model

Run on: February 24, 2004, 01:18:52 ; Search time 157.972 Seconds
                                              (without alignments)
                                              3316.252 Million cell updates/sec

Title: US-10-017-471B-19_COPY_1199_2142
Perfect score: 944
Sequence: 1 tcagccggagaacgcggggc..........caaaactactgcttcgggca 944

Scoring table: IDENTITY_NUC
                  Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Issued_Patents_NA:*
                  1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
                  2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
                  3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
                  4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
                  5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
                  6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES
                         %
Result   Query
    No.   Score   Match Length DB   ID   Description
    ----
c   1   58.4   6.2   933   4   US-09-084-669-1   Sequence 1, Appli
c   2   57.8   6.1   1908   1   US-08-173-508-1   Sequence 1, Appli
c   3   57.8   6.1   1908   2   US-08-265-310-1   Sequence 1, Appli
c   4   57.8   6.1   1908   3   US-08-951-742-1   Sequence 1, Appli
     5   56.8   6.0   1910   5   PCT-US92-05532-1   Sequence 1, Appli
     6   56.8   6.0   2261   1   US-08-272-882D-1   Sequence 1, Appli
c   7   55.6   5.9   1044   1   US-07-975-526-3   Sequence 3, Appli
c   8   55.6   5.9   1044   4   US-07-974-409C-425   Sequence 425, App
     9   55.6   5.9   30001   1   US-08-125-468-1   Sequence 1, Appli
    10   55.6   5.9   30001   2   US-08-474-933-1   Sequence 1, Appli
c   11   54.4   5.8   2634   3   US-08-941-936-1   Sequence 1, Appli
c   12   53.6   5.7   13842   3   US-09-105-537-30   Sequence 30, Appl

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OM nucleic - nucleic search, using sw model

Run on: February 24, 2004, 02:55:38 ; Search time 2565.84 Seconds
                                            (without alignments)
                                            1288.292 Million cell updates/sec

Title: US-10-017-471B-19_COPY_1199_2142
Perfect score: 944
Sequence: 1 tcagccggagaacgcggggc..........caaaactactgcttcgggca 944

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 2308684 seqs, 1750822206 residues

Total number of hits satisfying chosen parameters: 4617368

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Published_Applications_NA:*
                 1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
                 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
                 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
                 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
                 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
                 6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
                 7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
                 8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
                 9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
                 10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
                 11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
                 12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
                 13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
                 14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
                 15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
                 16: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
                 17: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
                 18: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

     Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being printed,
     and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	944	100.0	4346	14	US-10-017-471A-19	Sequence 19, Appl
	2	170	18.0	401	14	US-10-017-471A-12	Sequence 12, Appl
c	3	170	18.0	401	14	US-10-017-471A-13	Sequence 13, Appl
c	4	121.4	12.9	1035	14	US-10-156-761-2256	Sequence 2256, Ap
	5	121.4	12.9	9025608	14	US-10-156-761-1	Sequence 1, Appli
c	6	69.4	7.4	2817	14	US-10-156-761-390	Sequence 390, App
c	7	69.4	7.4	9025608	14	US-10-156-761-1	Sequence 1, Appli
c	8	68.8	7.3	4725	14	US-10-205-032-17	Sequence 17, Appl
c	9	68.8	7.3	60196	14	US-10-205-032-1	Sequence 1, Appli
c	10	67	7.1	15738	14	US-10-329-079-46	Sequence 46, Appl
c	11	67	7.1	61944	14	US-10-329-079-34	Sequence 34, Appl
c	12	62.8	6.7	88421	9	US-09-976-059-1	Sequence 1, Appli
c	13	62.2	6.6	1674	15	US-10-369-493-31436	Sequence 31436, A
c	14	61.6	6.5	1869	14	US-10-156-761-6969	Sequence 6969, Ap
c	15	61.2	6.5	15738	14	US-10-329-079-12	Sequence 12, Appl
c	16	61.2	6.5	37360	14	US-10-329-079-6	Sequence 6, Appli
c	17	61	6.5	1296	14	US-10-156-761-3664	Sequence 3664, Ap
c	18	60.6	6.4	2406	15	US-10-369-493-42365	Sequence 42365, A
c	19	60.4	6.4	1200	14	US-10-156-761-6339	Sequence 6339, Ap
c	20	58.4	6.2	903	14	US-10-121-988-81	Sequence 81, Appl
c	21	58.4	6.2	903	14	US-10-200-562-81	Sequence 81, Appl
c	22	58.4	6.2	903	14	US-10-237-551-81	Sequence 81, Appl
c	23	58.4	6.2	927	14	US-10-121-988-83	Sequence 83, Appl
c	24	58.4	6.2	927	14	US-10-200-562-83	Sequence 83, Appl
c	25	58.4	6.2	927	14	US-10-237-551-83	Sequence 83, Appl
	26	58.4	6.2	154746	10	US-09-827-688-8	Sequence 8, Appli
c	27	58.2	6.2	1942	12	US-10-282-122A-14251	Sequence 14251, A
c	28	58	6.1	1227	14	US-10-156-761-7107	Sequence 7107, Ap
c	29	58	6.1	2436	14	US-10-156-761-7456	Sequence 7456, Ap
c	30	57.8	6.1	31263	12	US-10-282-122A-25447	Sequence 25447, A
	31	57.6	6.1	897	14	US-10-156-761-6477	Sequence 6477, Ap
c	32	57.4	6.1	2223	14	US-10-156-761-7068	Sequence 7068, Ap
c	33	57	6.0	1182	14	US-10-156-761-1195	Sequence 1195, Ap
	34	57	6.0	2601	14	US-10-156-761-391	Sequence 391, App
c	35	57	6.0	10002	12	US-10-282-122A-14471	Sequence 14471, A
c	36	57	6.0	135638	14	US-10-314-657-1	Sequence 1, Appli
c	37	56.8	6.0	1284	14	US-10-156-761-6164	Sequence 6164, Ap
	38	56.8	6.0	2934	14	US-10-156-761-3186	Sequence 3186, Ap
c	39	56.2	6.0	3282	14	US-10-156-761-3885	Sequence 3885, Ap
c	40	56.2	6.0	4833	12	US-10-282-122A-25605	Sequence 25605, A
c	41	55.8	5.9	1767	14	US-10-156-761-4150	Sequence 4150, Ap
	42	55.6	5.9	1059	15	US-10-369-493-42237	Sequence 42237, A
c	43	55.6	5.9	1891	9	US-09-969-708-146	Sequence 146, App
c	44	55.6	5.9	1891	14	US-10-007-926A-234	Sequence 234, App
	45	55.2	5.8	1554	12	US-10-282-122A-14450	Sequence 14450, A

ALIGNMENTS

RESULT 1
US-10-017-471A-19

5.1.6

OM nucleic - nucleic search, using sw model

Run on: February 24, 2004, 01:18:08 ; Search time 6006.75 Seconds
                                    (without alignments)
                                    4693.036 Million cell updates/sec

Title: US-10-017-471B-19_COPY_1199_2142
Perfect score: 944
Sequence: 1 tcagccggagaacgcgggggc..........caaaactactgcttcgggca 944

Scoring table: IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   EST:*
                1: em_estba:*
                2: em_esthum:*
                3: em_estin:*
                4: em_estmu:*
                5: em_estov:*
                6: em_estpl:*
                7: em_estro:*
                8: em_htc:*
                9: gb_est1:*
                10: gb_est2:*
                11: gb_htc:*
                12: gb_est3:*
                13: gb_est4:*
                14: gb_est5:*
                15: em_estfun:*
                16: em_estom:*
                17: em_gss_hum:*
                18: em_gss_inv:*
                19: em_gss_pln:*
                20: em_gss_vrt:*
                21: em_gss_fun:*
                22: em_gss_mam:*
                23: em_gss_mus:*
                24: em_gss_pro:*
                25: em_gss_rod:*
                26: em_gss_phg:*
                27: em_gss_vrl:*
                28: gb_gss1:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	97.6	10.3	982	13	BX415111	BX415111 BX415111
	2	81.2	8.6	976	29	AG030647	AG030647 Pan trogl
	3	79	8.4	925	29	CNS0091P	AL053013 Drosophil
c	4	78.6	8.3	1421	28	BZ569488	BZ569488 pacs2-164
c	5	75.8	8.0	925	29	CNS0091P	AL053013 Drosophil
c	6	75.8	8.0	982	13	BX415111	BX415111 BX415111
c	7	75.6	8.0	1452	29	AG032979	AG032979 Pan trogl
c	8	75.2	8.0	1341	29	AG030611	AG030611 Pan trogl
c	9	75.2	8.0	1798	29	AG171124	AG171124 Pan trogl
c	10	74.8	7.9	1070	28	BZ557810	BZ557810 pacs1-60_
	11	73.8	7.8	932	29	CNS0072Q	AL066742 Drosophil
c	12	73.6	7.8	1073	14	CK209412	CK209412 FGAS02117
c	13	73.2	7.8	1299	29	AG039481	AG039481 Pan trogl
c	14	73	7.7	1165	29	AG030649	AG030649 Pan trogl
c	15	72.8	7.7	1189	29	AG030608	AG030608 Pan trogl
	16	72.8	7.7	1598	29	AG030579	AG030579 Pan trogl
	17	72.6	7.7	1370	29	AG072551	AG072551 Pan trogl
c	18	72	7.6	1143	13	BU502934	BU502934 AGENCOURT
c	19	71.6	7.6	1088	29	AG075424	AG075424 Pan trogl
	20	71	7.5	796	28	AZ192927	AZ192927 SP_1022_B
	21	70.8	7.5	1069	13	BQ675554	BQ675554 AGENCOURT
c	22	70.8	7.5	1277	29	AG060206	AG060206 Pan trogl
	23	70.4	7.5	1250	29	AG043469	AG043469 Pan trogl
c	24	70	7.4	935	29	CNS006XK	AL066051 Drosophil
c	25	70	7.4	1040	12	BG786331	BG786331 SEAUMC006
c	26	69.8	7.4	932	29	CNS0072Q	AL066742 Drosophil
c	27	69.6	7.4	1203	29	CNS015Y4	AL106054 Drosophil
	28	69.2	7.3	924	13	BX442207	BX442207 BX442207
	29	69.2	7.3	1278	29	AG060116	AG060116 Pan trogl
	30	69.2	7.3	1299	29	AG039481	AG039481 Pan trogl
c	31	69	7.3	1278	29	AG060116	AG060116 Pan trogl
c	32	68.8	7.3	1065	13	BQ681076	BQ681076 AGENCOURT
	33	68.6	7.3	935	29	CNS006XK	AL066051 Drosophil
c	34	68.6	7.3	1369	29	AG081191	AG081191 Pan trogl
c	35	68.4	7.2	840	29	AG043467	AG043467 Pan trogl
	36	68.4	7.2	1856	29	AG072699	AG072699 Pan trogl
c	37	67.8	7.2	1305	12	BM903696	BM903696 AGENCOURT
c	38	67.4	7.1	1135	13	BU506367	BU506367 AGENCOURT
	39	67.2	7.1	1002	29	AG146122	AG146122 Pan trogl
	40	67	7.1	1057	29	CNS046BO	AL276477 Tetraodon
	41	66.8	7.1	1017	29	AG058770	AG058770 Pan trogl
c	42	66.8	7.1	1026	28	BZ569417	BZ569417 pacs2-164
c	43	66.8	7.1	1094	29	AG036373	AG036373 Pan trogl
	44	66.8	7.1	1341	29	AG030611	AG030611 Pan trogl
c	45	66.6	7.1	1038	29	AG060254	AG060254 Pan trogl

```
                        GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on:          February 24, 2004, 08:03:40 ; Search time 3439 Seconds
                                              (without alignments)
                                              3944.859 Million cell updates/sec

Title:           US-10-017-471B-17
Perfect score:   1645
Sequence:        1 MPEAVVLINSASDANSIEQT.........GHQDGSLVFLTTLSGPAFSG 313


Scoring table:   BLOSUM62
                 Xgapop 10.0 , Xgapext  0.5
                 Ygapop 10.0 , Ygapext  0.5
                 Fgapop  6.0 , Fgapext  7.0
                 Delop   6.0 , Delext   7.0


Searched:        3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters:      6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
```

SEQ 17 (protein) in DNA databases

```
Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlp
-
Q=/cgn2_1/USPTO_spool_p/US10017471/runat_23022004_101401_28710/app_query.fasta_1
.455
-DB=GenEmbl -QFMT=fastap -SUFFIX=rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10017471_@CGN_1_1_5265_@runat_23022004_101401_28710 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :       GenEmbl:*
                 1:  gb_ba:*
                 2:  gb_htg:*
                 3:  gb_in:*
                 4:  gb_om:*
                 5:  gb_ov:*
                 6:  gb_pat:*
                 7:  gb_ph:*
                 8:  gb_pl:*
                 9:  gb_pr:*
                 10:  gb_ro:*
                 11:  gb_sts:*
```

```
12:   gb_sy:*
13:   gb_un:*
14:   gb_vi:*
15:   em_ba:*
16:   em_fun:*
17:   em_hum:*
18:   em_in:*
19:   em_mu:*
20:   em_om:*
21:   em_or:*
22:   em_ov:*
23:   em_pat:*
24:   em_ph:*
25:   em_pl:*
26:   em_ro:*
27:   em_sts:*
28:   em_un:*
29:   em_vi:*
30:   em_htg_hum:*
31:   em_htg_inv:*
32:   em_htg_other:*
33:   em_htg_mus:*
34:   em_htg_pln:*
35:   em_htg_rod:*
36:   em_htg_mam:*
37:   em_htg_vrt:*
38:   em_sy:*
39:   em_htgo_hum:*
40:   em_htgo_mus:*
41:   em_htgo_other:*
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

<div align="center">SUMMARIES</div>

Result No.	Score	% Query Match	Length	DB	ID	Description
c 1	1634.5	99.4	6727	1	SCO007731	AJ007731 Streptomy
2	1634.5	99.4	290850	1	SCO939127	AL939127 Streptomy
3	1050.5	63.9	1203	1	STMAFSAA	M24250 S.griseus a
4	1050.5	63.9	12070	1	AB011413	AB011413 Streptomy
5	617	37.5	6252	1	SVU24659	U24659 Streptomyce
6	562.5	34.2	1215	1	AB001608	AB001608 Streptomy
7	524.5	31.9	210614	1	AB088224	AB088224 Streptomy
8	510	31.0	92294	1	AY117439	AY117439 Streptomy
9	483.5	29.4	2234	1	AB001683	AB001683 Streptomy
c 10	319.5	19.4	300550	1	AP005030	AP005030 Streptomy
c 11	271.5	16.5	9521	6	AX188771	AX188771 Sequence
12	271.5	16.5	9521	6	AX188772	AX188772 Sequence
c 13	271.5	16.5	22918	1	SCO276673	AJ276673 Streptomy
14	271.5	16.5	178073	1	SCO590464	AL590464 Streptomy
c 15	132	8.0	303400	1	AP006578	AP006578 Gloeobact
c 16	131	8.0	1755	1	STMBARA	D32251 Streptomyce
c 17	124.5	7.6	11426	1	AY271660	AY271660 Actinomad

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OM protein - nucleic search, using frame_plus_p2n model

Run on: February 24, 2004, 07:58:09 ; Search time 397 Seconds
                                              (without alignments)
                                              3349.335 Million cell updates/sec

Title: US-10-017-471B-17
Perfect score: 1645
Sequence: 1 MPEAVVLINSASDANSIEQT..........GHQDGSLVFLTTLSGPAFSG 313

Scoring table: BLOSUM62
                 Xgapop 10.0 , Xgapext 0.5
                 Ygapop 10.0 , Ygapext 0.5
                 Fgapop 6.0 , Fgapext 7.0
                 Delop   6.0 , Delext   7.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlp

Q=/cgn2_1/USPTO_spool_p/US10017471/runat_23022004_101401_28700/app_query.fasta_1
.455
-DB=N_Geneseq_29Jan04 -QFMT=fastap -SUFFIX=rng -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10017471_@CGN_1_1_708_@runat_23022004_101401_28700 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :   N_Geneseq_29Jan04:*
                 1: geneseqn1980s:*
                 2: geneseqn1990s:*
                 3: geneseqn2000s:*
                 4: geneseqn2001as:*
                 5: geneseqn2001bs:*
                 6: geneseqn2002s:*
                 7: geneseqn2003as:*
                 8: geneseqn2003bs:*
                 9: geneseqn2003cs:*
                 10: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
c	1	1634.5	99.4	4346	6	ABN86379	Abn86379 ScbA, Scb
c	2	1634.5	99.4	4346	9	ADE14794	Ade14794 Streptomy
c	3	288	17.5	401	6	ABN86377	Abn86377 S. coelic
	4	288	17.5	401	6	ABN86378	Abn86378 S. coelic
c	5	288	17.5	401	9	ADE14790	Ade14790 Streptomy
c	6	271.5	16.5	9521	4	AAS07627	Aas07627 Streptoco
	7	126	7.7	3206	9	ADC30782	Adc30782 Human nov
	8	122	7.4	2971	5	AAS84741	Aas84741 DNA encod
	9	120	7.3	2492	9	ADD47157	Add47157 Human gen
	10	120	7.3	2492	9	ADE57663	Ade57663 Human gen
	11	120	7.3	2492	9	ADE57659	Ade57659 Human gen
	12	120	7.3	2492	9	ADD47153	Add47153 Human gen
c	13	119	7.2	2927	9	ADE59463	Ade59463 Human gen
	14	118.5	7.2	3131	9	ADC30783	Adc30783 Human nov
c	15	118.5	7.2	28000	9	ADD00956	Add00956 Human Jag
	16	115	7.0	1647	6	ABQ90156	Abq90156 M. capsul
	17	111.5	6.8	28598	2	AAT06769	Aat06769 Sorangium
	18	111.5	6.8	28958	2	AAT89956	Aat89956 Sorangium
	19	111.5	6.8	28958	3	AAA75299	Aaa75299 DNA seque
	20	111.5	6.8	49377	2	AAV05287	Aav05287 The sorap
c	21	109.5	6.7	5576	7	ACC48897	Acc48897 Rhodococc
c	22	109.5	6.7	23656	7	ACC48894	Acc48894 Rhodococc
c	23	108.5	6.6	77536	3	AAA14651	Aaa14651 Nucleotid
c	24	108	6.6	110000	4	AAI99682_38	Continuation (39 o
c	25	108	6.6	110000	4	AAI99683_38	Continuation (39 o
	26	108	6.6	135638	7	ABX34289	Abx34289 S. atrool
c	27	107.5	6.5	110000	4	AAI99683_20	Continuation (21 o
	28	107	6.5	10763	2	AAV39837	Aav39837 Pseudomon
	29	107	6.5	10763	2	AAX99368	Aax99368 P. fluore
c	30	107	6.5	110000	4	AAI99682_20	Continuation (21 o
	31	105.5	6.4	2081	2	AAV01452	Aav01452 Modified
	32	105.5	6.4	3196	2	AAV01447	Aav01447 Daunomyci
c	33	105.5	6.4	6491	6	ABA97234	Aba97234 pcu opero
c	34	105.5	6.4	6491	7	ACA92456	Aca92456 Pseudomon
	35	105	6.4	1384	4	AAS32671	Aas32671 Human gen
c	36	105	6.4	1644	9	ADC30402	Adc30402 Human nov
	37	104.5	6.4	3013	2	AAV01451	Aav01451 Plasmid p
	38	104.5	6.4	3196	2	AAV01453	Aav01453 Streptomy
c	39	104.5	6.4	3763	10	ADE77078	Ade77078 Human cDN
c	40	104.5	6.4	9975	7	AAL61173	Aal61173 Actinosyn
c	41	104.5	6.4	28598	2	AAT06769	Aat06769 Sorangium
c	42	104.5	6.4	28958	2	AAT89956	Aat89956 Sorangium
c	43	104.5	6.4	28958	3	AAA75299	Aaa75299 DNA seque
c	44	104.5	6.4	40123	9	ADB74388	Adb74388 Mycobacte
c	45	104.5	6.4	49377	2	AAV05287	Aav05287 The sorap

ALIGNMENTS

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OM protein - nucleic search, using frame_plus_p2n model

Run on: February 24, 2004, 08:14:27 ; Search time 90 Seconds
                                      (without alignments)
                                      1929.996 Million cell updates/sec

Title: US-10-017-471B-17
Perfect score: 1645
Sequence: 1 MPEAVVLINSASDANSIEQT.........GHQDGSLVFLTTLSGPAFSG 313

Scoring table: BLOSUM62
                 Xgapop 10.0 , Xgapext 0.5
                 Ygapop 10.0 , Ygapext 0.5
                 Fgapop 6.0 , Fgapext 7.0
                 Delop   6.0 , Delext   7.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlp
-
Q=/cgn2_1/USPTO_spool_p/US10017471/runat_23022004_101402_28736/app_query.fasta_1
.455
-DB=Issued_Patents_NA -QFMT=fastap -SUFFIX=rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10017471_@CGN_1_1_85_@runat_23022004_101402_28736 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :   Issued_Patents_NA:*
                 1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
                 2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
                 3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
                 4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
                 5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
                 6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

```
                                    SUMMARIES
                         %
        Result          Query
           No.    Score  Match Length DB   ID                        Description
        ------------------------------------------------------------------------------
            1    115.5    7.0    2127   4   US-09-252-991A-1503        Sequence 1503, Ap
            2    111.5    6.8   28958   1   US-08-258-261B-6           Sequence 6, Appli
            3    111.5    6.8   28958   1   US-08-456-837-6            Sequence 6, Appli
            4    111.5    6.8   28958   1   US-08-457-342-6            Sequence 6, Appli
            5    111.5    6.8   28958   1   US-08-457-646A-6           Sequence 6, Appli
            6    111.5    6.8   28958   1   US-08-458-076A-6           Sequence 6, Appli
            7    111.5    6.8   28958   1   US-08-764-233A-4           Sequence 4, Appli
            8    111.5    6.8   28958   1   US-08-457-335A-6           Sequence 6, Appli
            9    111.5    6.8   28958   1   US-08-729-214-6            Sequence 6, Appli
           10    111.5    6.8   28958   3   US-09-028-934-6            Sequence 6, Appli
           11    111.5    6.8   49377   1   US-08-764-233A-1           Sequence 1, Appli
           12    110      6.7    2250   4   US-09-252-991A-4181        Sequence 4181, Ap
    c      13    108.5    6.6   77536   4   US-09-410-551B-1           Sequence 1, Appli
    c      14    108      6.6 4403765   3   US-09-103-840A-2           Sequence 2, Appli
    c      15    108      6.6 4411529   3   US-09-103-840A-1           Sequence 1, Appli
    c      16    107      6.5    1251   4   US-09-489-039A-5971        Sequence 5971, Ap
           17    107      6.5    1443   4   US-09-252-991A-10228       Sequence 10228, A
           18    107      6.5   10763   1   US-08-761-258-1            Sequence 1, Appli
           19    107      6.5   10763   2   US-08-977-306-1            Sequence 1, Appli
    c      20    106.5    6.5    1266   4   US-09-252-991A-10804       Sequence 10804, A
    c      21    106      6.4    2730   4   US-09-489-039A-6744        Sequence 6744, Ap
           22    105.5    6.4    2081   2   US-09-096-982-7            Sequence 7, Appli
           23    105.5    6.4    2081   2   US-08-653-650A-7           Sequence 7, Appli
           24    105.5    6.4    3196   2   US-09-096-982-4            Sequence 4, Appli
           25    105.5    6.4    3196   2   US-08-653-650A-4           Sequence 4, Appli
    c      26    105.5    6.4    6491   4   US-09-585-174-1            Sequence 1, Appli
    c      27    104.5    6.4    2130   4   US-09-489-039A-3847        Sequence 3847, Ap
           28    104.5    6.4    3013   2   US-09-096-982-6            Sequence 6, Appli
           29    104.5    6.4    3013   2   US-08-653-650A-6           Sequence 6, Appli
    c      30    104.5    6.4    5185   4   US-09-976-594-640          Sequence 640, App
    c      31    104.5    6.4   28958   1   US-08-258-261B-6           Sequence 6, Appli
    c      32    104.5    6.4   28958   1   US-08-456-837-6            Sequence 6, Appli
    c      33    104.5    6.4   28958   1   US-08-457-342-6            Sequence 6, Appli
    c      34    104.5    6.4   28958   1   US-08-457-646A-6           Sequence 6, Appli
    c      35    104.5    6.4   28958   1   US-08-458-076A-6           Sequence 6, Appli
    c      36    104.5    6.4   28958   1   US-08-764-233A-4           Sequence 4, Appli
    c      37    104.5    6.4   28958   1   US-08-457-335A-6           Sequence 6, Appli
    c      38    104.5    6.4   28958   1   US-08-729-214-6            Sequence 6, Appli
    c      39    104.5    6.4   28958   3   US-09-028-934-6            Sequence 6, Appli
    c      40    104.5    6.4   40123   4   US-08-311-731A-137         Sequence 137, App
    c      41    104.5    6.4   49377   1   US-08-764-233A-1           Sequence 1, Appli
           42    104.5    6.4 4403765   3   US-09-103-840A-2           Sequence 2, Appli
           43    104.5    6.4 4411529   3   US-09-103-840A-1           Sequence 1, Appli
           44    104      6.3    1206   4   US-09-252-991A-16406       Sequence 16406, A
           45    104      6.3    1983   4   US-09-252-991A-16300       Sequence 16300, A


                                    ALIGNMENTS


RESULT 1
US-09-252-991A-1503
; Sequence 1503, Application US/09252991A
```

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OM protein - nucleic search, using frame_plus_p2n model

Run on: February 24, 2004, 09:26:05 ; Search time 383 Seconds
                                             (without alignments)
                                             2861.657 Million cell updates/sec

Title: US-10-017-471B-17
Perfect score: 1645
Sequence: 1 MPEAVVLINSASDANSIEQT.........GHQDGSLVFLTTLSGPAFSG 313

Scoring table: BLOSUM62
                 Xgapop 10.0 , Xgapext 0.5
                 Ygapop 10.0 , Ygapext 0.5
                 Fgapop 6.0 , Fgapext 7.0
                 Delop   6.0 , Delext   7.0

Searched: 2308684 seqs, 1750822206 residues

Total number of hits satisfying chosen parameters: 4617368

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlp

Q=/cgn2_1/USPTO_spool_p/US10017471/runat_23022004_101404_28819/app_query.fasta_1
.455
-DB=Published_Applications_NA -QFMT=fastap -SUFFIX=rnpb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US10017471_@CGN_1_1_333_@runat_23022004_101404_28819
-NCPU=6 -ICPU=3 -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :   Published_Applications_NA:*
                 1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
                 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
                 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
                 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
                 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
                 6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
                 7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
                 8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
                 9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
                 10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
                 11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*

```
12:  /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
13:  /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
14:  /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
15:  /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
16:  /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
17:  /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
18:  /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
c	1	1634.5	99.4	4346	14	US-10-017-471A-19	Sequence 19, Appl
	2	319.5	19.4	1035	14	US-10-156-761-2256	Sequence 2256, Ap
c	3	319.5	19.4	9025608	14	US-10-156-761-1	Sequence 1, Appli
c	4	288	17.5	401	14	US-10-017-471A-12	Sequence 12, Appl
	5	288	17.5	401	14	US-10-017-471A-13	Sequence 13, Appl
	6	118.5	7.2	2918	14	US-10-171-581-74	Sequence 74, Appl
c	7	118.5	7.2	28000	14	US-10-091-625-11	Sequence 11, Appl
c	8	118.5	7.2	28000	14	US-10-096-399A-11	Sequence 11, Appl
c	9	118.5	7.2	28000	15	US-10-461-668-11	Sequence 11, Appl
c	10	118.5	7.2	28000	15	US-10-388-263-381	Sequence 381, App
c	11	112.5	6.8	4062	14	US-10-156-761-875	Sequence 875, App
	12	110.5	6.7	9025608	14	US-10-156-761-1	Sequence 1, Appli
c	13	109.5	6.7	1053	14	US-10-156-761-6354	Sequence 6354, Ap
	14	108.5	6.6	1219	15	US-10-374-780A-1144	Sequence 1144, Ap
c	15	108.5	6.6	77536	10	US-09-940-316B-1	Sequence 1, Appli
c	16	108	6.6	1704	14	US-10-156-761-963	Sequence 963, App
	17	108	6.6	135638	14	US-10-314-657-1	Sequence 1, Appli
	18	107.5	6.5	1101	15	US-10-369-493-31782	Sequence 31782, A
c	19	106.5	6.5	1785	14	US-10-156-761-3032	Sequence 3032, Ap
c	20	105.5	6.4	6491	9	US-09-997-664-1	Sequence 1, Appli
c	21	105.5	6.4	6491	15	US-10-464-952-1	Sequence 1, Appli
	22	105	6.4	1384	15	US-10-074-024-625	Sequence 625, App
	23	104.5	6.4	1821	14	US-10-156-761-1824	Sequence 1824, Ap
c	24	104.5	6.4	3763	10	US-09-919-039-243	Sequence 243, App
	25	104	6.3	13559	14	US-10-133-013-123	Sequence 123, App
	26	104	6.3	13793	15	US-10-159-563-110	Sequence 110, App
c	27	104	6.3	14427	14	US-10-156-761-1540	Sequence 1540, Ap
c	28	103.5	6.3	1120	16	US-10-294-445-22	Sequence 22, Appl
c	29	103.5	6.3	2166	12	US-10-282-122A-14878	Sequence 14878, A
	30	103	6.3	1137	14	US-10-156-761-1695	Sequence 1695, Ap
c	31	103	6.3	1248	14	US-10-156-761-1741	Sequence 1741, Ap
	32	103	6.3	1821	12	US-10-282-122A-26234	Sequence 26234, A
	33	103	6.3	1875	12	US-10-282-122A-28693	Sequence 28693, A
	34	103	6.3	3285	14	US-10-228-063-46	Sequence 46, Appl
c	35	103	6.3	4974	14	US-10-156-761-2487	Sequence 2487, Ap
	36	102.5	6.2	1219	15	US-10-369-493-35271	Sequence 35271, A
	37	102.5	6.2	1219	15	US-10-369-493-38541	Sequence 38541, A
	38	102.5	6.2	1219	15	US-10-369-493-38730	Sequence 38730, A
c	39	102.5	6.2	1803	14	US-10-156-761-3571	Sequence 3571, Ap
c	40	102.5	6.2	2076	12	US-10-282-122A-23281	Sequence 23281, A

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OM protein - nucleic search, using frame_plus_p2n model

Run on: February 24, 2004, 08:03:55 ; Search time 2549 Seconds
                                              (without alignments)
                                              3666.874 Million cell updates/sec

Title: US-10-017-471B-17
Perfect score: 1645
Sequence: 1 MPEAVVLINSASDANSIEQT..........GHQDGSLVFLTTLSGPAFSG 313

Scoring table: BLOSUM62
                 Xgapop 10.0 , Xgapext 0.5
                 Ygapop 10.0 , Ygapext 0.5
                 Fgapop 6.0 , Fgapext 7.0
                 Delop   6.0 , Delext   7.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlp
-
Q=/cgn2_1/USPTO_spool_p/US10017471/runat_23022004_101402_28722/app_query.fasta_1
.455
-DB=EST -QFMT=fastap -SUFFIX=rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10017471_@CGN_1_1_4237_@runat_23022004_101402_28722 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :   EST:*
                 1:   em_estba:*
                 2:   em_esthum:*
                 3:   em_estin:*
                 4:   em_estmu:*
                 5:   em_estov:*
                 6:   em_estpl:*
                 7:   em_estro:*
                 8:   em_htc:*
                 9:   gb_est1:*
                 10: gb_est2:*
                 11: gb_htc:*

```
12:  gb_est3:*
13:  gb_est4:*
14:  gb_est5:*
15:  em_estfun:*
16:  em_estom:*
17:  em_gss_hum:*
18:  em_gss_inv:*
19:  em_gss_pln:*
20:  em_gss_vrt:*
21:  em_gss_fun:*
22:  em_gss_mam:*
23:  em_gss_mus:*
24:  em_gss_pro:*
25:  em_gss_rod:*
26:  em_gss_phg:*
27:  em_gss_vrl:*
28:  gb_gss1:*
29:  gb_gss2:*
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	125	7.6	1001	13	BQ056725	BQ056725 AGENCOURT
2	125	7.6	1086	13	BQ054980	BQ054980 AGENCOURT
3	123.5	7.5	1003	13	BQ056011	BQ056011 AGENCOURT
4	121.5	7.4	975	13	BQ060965	BQ060965 AGENCOURT
5	121.5	7.4	1051	13	BQ716861	BQ716861 AGENCOURT
6	121	7.4	1032	13	BQ069797	BQ069797 AGENCOURT
7	121	7.4	1060	12	BM909582	BM909582 AGENCOURT
8	120.5	7.3	921	13	BQ055424	BQ055424 AGENCOURT
9	120	7.3	940	13	BQ061849	BQ061849 AGENCOURT
10	120	7.3	947	13	BQ064227	BQ064227 AGENCOURT
11	120	7.3	948	13	BQ064307	BQ064307 AGENCOURT
12	120	7.3	984	13	BQ058735	BQ058735 AGENCOURT
13	120	7.3	986	13	BQ057095	BQ057095 AGENCOURT
14	120	7.3	990	13	BQ065162	BQ065162 AGENCOURT
15	120	7.3	991	13	BQ060878	BQ060878 AGENCOURT
16	120	7.3	1010	13	BQ059796	BQ059796 AGENCOURT
17	120	7.3	1037	13	BQ058702	BQ058702 AGENCOURT
18	120	7.3	1061	13	BQ061532	BQ061532 AGENCOURT
19	119.5	7.3	1054	13	BQ062294	BQ062294 AGENCOURT
20	119	7.2	930	13	BQ642458	BQ642458 AGENCOURT
21	119	7.2	1062	13	BQ062693	BQ062693 AGENCOURT
22	119	7.2	1067	13	BQ054981	BQ054981 AGENCOURT
23	118.5	7.2	883	29	CG232584	CG232584 OGWGZ16TV
24	118	7.2	552	14	CF135436	CF135436 UI-HF-BR0
25	118	7.2	725	14	CF125660	CF125660 UI-HF-EL0
26	118	7.2	862	13	BQ705954	BQ705954 AGENCOURT
27	118	7.2	1000	13	BQ071526	BQ071526 AGENCOURT
28	118	7.2	1051	12	BQ054446	BQ054446 AGENCOURT
29	117	7.1	1006	13	BQ068456	BQ068456 AGENCOURT